

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 09/117,246C
Source: ITW16
Date Processed by STIC: 3/8/06

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/117,246C

DATE: 03/08/2006

TIME: 11:53:26

Input Set : A:\.txt

Output Set: N:\CRF4\03072006\I117246C.raw

3 <110> APPLICANT: Ludevid, Dolores
 4 Torrent, Margarita
 5 Alvarez, Inaki
 6 Perez, Pascual
 8 <120> TITLE OF INVENTION: Amino acid-enriched plant protein reserves, particularly
 9 lysine-enriched maize-zein, and plants expressing such proteins
 11 <130> FILE REFERENCE: 50062/004001
 13 <140> CURRENT APPLICATION NUMBER: US 09/117,246C
 14 <141> CURRENT FILING DATE: 1998-12-03
 16 <150> PRIOR APPLICATION NUMBER: PCT/FR97/00167
 17 <151> PRIOR FILING DATE: 1997-01-28
 19 <150> PRIOR APPLICATION NUMBER: FR96/01004
 20 <151> PRIOR FILING DATE: 1996-01-29
 22 <160> NUMBER OF SEQ ID NOS: 24
 24 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 44
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: based on Maize
 34 <400> SEQUENCE: 1
 35 cgatgaattc aaaccaaagg caaagccgaa gccaaaagaa ttca 44
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 46
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: based on Maize
 46 <400> SEQUENCE: 2
 47 agcttgaatt cttttggctt cggctttggc tttgggttga attcat 46
 50 <210> SEQ ID NO: 3
 51 <211> LENGTH: 17
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Maize
 55 <400> SEQUENCE: 3
 57 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln
 58 1 5 10 15
 61 Pro
 65 <210> SEQ ID NO: 4
 66 <211> LENGTH: 28
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Maize

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70 <400> SEQUENCE: 4
72 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro
73 1 5 10 15
76 Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln Pro
77 20 25
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 20
82 <212> TYPE: PRT
83 <213> ORGANISM: Maize
85 <400> SEQUENCE: 5
87 Asp Gly Ile Asp Glu Phe Lys Pro Lys Pro Lys Pro Lys Glu
88 1 5 10 15
91 Phe Lys Leu Asp
92 20
95 <210> SEQ ID NO: 6
96 <211> LENGTH: 672
97 <212> TYPE: DNA
98 <213> ORGANISM: Maize
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)..(672)
105 <400> SEQUENCE: 6
106 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
107 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Ala Ser
108 1 5 10 15
110 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
111 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
112 20 25 30
114 ccg gtt cat cta ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
115 Pro Val His Leu Pro Pro Val His Leu Pro Pro Pro Val His Leu
116 35 40 45
118 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
119 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
120 50 55 60
122 cac ctg cca ccg ccg gtc cat gtg ccg ccg gtt cat ctg ccg ccg 240
123 His Leu Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
124 65 70 75 80
126 cca cca tgc cac tac cct actcaa ccg ccc ccg cct cag cct cat ccc 288
127 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
128 85 90 95
130 cag cca cac cca tgc ccg tgc caa cag ccg cat cca agc ccg tgc cag 336
131 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
132 100 105 110
134 ctg cag gga acc tgc ggc gtt ggc agc acc ccg atc ctg ggc cag tgc 384
135 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
136 115 120 125
138 gtc gag ttt ctg agg cat cag tgc agc ccg acg gcg acg ccc tac tgc
139 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys 432
140 130 135 140

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142	tcg	cct	cag	tgc	cag	tcg	ttg	cg	cag	tgt	tgc	cag	cag	ctc	agg	480	
143	Ser	Pro	Gln	Cys	Gln	Ser	Leu	Arg	Gln	Gln	Cys	Cys	Gln	Gln	Leu	Arg	
144	145						150			155					160		
146	cag	gtg	gag	ccg	cag	cac	cg	tac	cag	g	atc	ttc	ggc	ttg	gtc	ctc	528
147	Gln	Val	Glu	Pro	Gln	His	Arg	Tyr	Gln	Ala	Ile	Phe	Gly	Leu	Val	Leu	
148							165			170					175		
150	cag	tcc	atc	ctg	cag	cag	ccg	caa	agc	ggc	cag	gtc	g	gg	ctg	576	
151	Gln	Ser	Ile	Leu	Gln	Gln	Gln	Pro	Gln	Ser	Gly	Gln	Val	Ala	Gly	Leu	
152							180			185					190		
154	ttg	g	cg	cag	ata	g	cg	cag	caa	ctg	ac	g	atg	tg	gg	ctg	624
155	Leu	Ala	Ala	Gln	Ile	Ala	Gln	Gln	Leu	Thr	Ala	Met	Cys	Gly	Leu	Gln	
156							195			200					205		
158	cag	ccg	act	cca	tgc	ccc	tac	gct	g	cc	gg	gt	gtc	ccc	cac	tga	672
159	Gln	Pro	Thr	Pro	Cys	Pro	Tyr	Ala	Ala	Gly	Gly	Val	Pro	His			
160							210			215					220		
163	<210> SEQ ID NO: 7																
164	<211> LENGTH: 223																
165	<212> TYPE: PRT																
166	<213> ORGANISM: Maize																
168	<400> SEQUENCE: 7																
170	Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Ala	Ala	Ser				
171	1				5			10			15						
174	Ala	Thr	Ser	Thr	His	Thr	Ser	Gly	Gly	Cys	Gly	Cys	Gln	Pro	Pro	Pro	
175					20			25			30						
178	Pro	Val	His	Leu	Pro	Pro	Pro	Val	His	Leu	Pro	Pro	Pro	Val	His	Leu	
179					35			40			45						
182	Pro	Pro	Pro	Val	His	Leu	Pro	Pro	Pro	Val	His	Leu	Pro	Pro	Pro	Val	
183					50			55			60						
186	His	Leu	Pro	Pro	Pro	Val	His	Val	Pro	Pro	Pro	Val	His	Leu	Pro	Pro	
187					65			70			75					80	
190	Pro	Pro	Cys	His	Tyr	Pro	Thr	Gln	Pro	Pro	Arg	Pro	Gln	Pro	His	Pro	
191					85			90			95						
194	Gln	Pro	His	Pro	Cys	Pro	Cys	Gln	Gln	Pro	His	Pro	Ser	Pro	Cys	Gln	
195					100			105			110						
198	Leu	Gln	Gly	Thr	Cys	Gly	Val	Gly	Ser	Thr	Pro	Ile	Leu	Gly	Gln	Cys	
199					115			120			125						
202	Val	Glu	Phe	Leu	Arg	His	Gln	Cys	Ser	Pro	Thr	Ala	Thr	Pro	Tyr	Cys	
203					130			135			140						
206	Ser	Pro	Gln	Cys	Gln	Ser	Leu	Arg	Gln	Gln	Cys	Cys	Gln	Gln	Leu	Arg	
207					145			150			155					160	
210	Gln	Val	Glu	Pro	Gln	His	Arg	Tyr	Gln	Ala	Ile	Phe	Gly	Leu	Val	Leu	
211					165			170			175						
214	Gln	Ser	Ile	Leu	Gln	Gln	Gln	Pro	Gln	Ser	Gly	Gln	Val	Ala	Gly	Leu	
215					180			185			190						
218	Leu	Ala	Ala	Gln	Ile	Ala	Gln	Gln	Leu	Thr	Ala	Met	Cys	Gly	Leu	Gln	
219					195			200			205						
222	Gln	Pro	Thr	Pro	Cys	Pro	Tyr	Ala	Ala	Ala	Gly	Gly	Val	Pro	His		
223					210			215			220						
226	<210> SEQ ID NO: 8																

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Input Set : A:\.txt
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227 <211> LENGTH: 693
228 <212> TYPE: DNA
229 <213> ORGANISM: maize
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (1)..(693)
236 <400> SEQUENCE: 8
237 atg agg gtg ttg ctc gtc ctc gct ctc ctg gct ctc gct gcg agc 48
238 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Ala Ser
239 1 5 10 15
241 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
242 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
243 20 25 30
245 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
246 Pro Val His Leu Pro Pro Val His Leu Pro Pro Pro Val His Leu
247 35 40 45
249 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
250 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
251 50 55 60
253 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg 240
254 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
255 65 70 75 80
257 cca cca tgc cac tac cct actcaa ccg ccc ccg atc gaa ttc aaa cca 288
258 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
259 85 90 95
261 aag cca aag ccg aag cca aaa gaa ttc aaa cca aag cca aag ccg aag 336
262 Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
263 100 105 110
265 cca aaa gaa ttc ctg cag ccc ctg cag gga acc tgc ggc gtt ggc agc 384
266 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
267 115 120 125
269 acc ccg atc ctg ggc cag tgc gtc gag ttt ctg agg cat cag tgc agc 432
270 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
271 130 135 140
273 ccg acg gcg acg ccc tac tgc tcg cct cag tgc cag tcg ttg ccg cag 480
274 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
275 145 150 155 160
277 cag tgt tgc cag cag ctc agg cag gtg gag ccg cag cac ccg tac cag 528
278 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
279 165 170 175
281 gcg atc ttc ggc ttg gtc ctc cag tcc atc ctg cag cag ccg caa 576
282 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
283 180 185 190
285 agc ggc cag gtc gcg ggg ctg ttg gcg gcg cag ata gcg cag caa ctg 624
286 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
287 195 200 205
289 acg gcg atg tgc ggc ctg cag cag ccg act cca tgc ccc tac gct gct 672
290 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
291 210 215 220

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293 gcc ggc ggt gtc ccc cac tga 693
 294 Ala Gly Gly Val Pro His
 295 225 230
 298 <210> SEQ ID NO: 9
 299 <211> LENGTH: 230
 300 <212> TYPE: PRT
 301 <213> ORGANISM: maize
 303 <400> SEQUENCE: 9
 305 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Ala Ala Ser
 306 1 5 10 15
 309 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
 310 20 25 30
 313 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
 314 35 40 45
 317 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
 318 50 55 60
 321 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
 322 65 70 75 80
 325 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
 326 85 90 95
 329 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
 330 100 105 110
 333 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
 334 115 120 125
 337 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
 338 130 135 140
 341 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
 342 145 150 155 160
 345 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
 346 165 170 175
 349 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
 350 180 185 190
 353 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
 354 195 200 205
 357 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
 358 210 215 220
 361 Ala Gly Gly Val Pro His
 362 225 230
 365 <210> SEQ ID NO: 10
 366 <211> LENGTH: 723
 367 <212> TYPE: DNA
 368 <213> ORGANISM: Maize
 371 <220> FEATURE:
 372 <221> NAME/KEY: CDS
 373 <222> LOCATION: (1)..(723)
 375 <400> SEQUENCE: 10
 376 atg agg gtg ttg ctc gtc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
 377 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Leu Ala Ala Ser
 378 1 5 10 15

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

o of n and/or Xaa have been detected in the Sequence Listing. Please review the
quence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

:#:22; Xaa Pos. 5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25
:#:22; Xaa Pos. 26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44
:#:22; Xaa Pos. 45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60

VERIFICATION SUMMARY

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349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0

341 Repeated in SeqNo=22